

#4

		2661		2730
humPMS2	(2574)	CAATTCTCAGAC		
AtPMS2	(2267)	CTTAACTCCTTTACCTGATGACGACAATGTCAATGATGATGATGATGATGCAACCATCTCATGGC		
Consensus	(2661)	C TT CTCA A		
		2731		
humPMS2	(2587)	----		
AtPMS2	(2337)	ATGA		
Consensus	(2731)			

FIG. 1

FIG. 1

humPMS2	(1)	-----VERAESSS-----EPAKAKPIIDRKSCHOCSSQVLSLSTAVKELVENSLSAGATNIDL	70
AtMLH1	(1)	MIDSSSLTARVEEESPAITIVPREPPKORLEESVNRFAEPHIQRPVSAYKELVENSLSDESSSSSV	
Consensus	(1)	ME ES AT I ID V I AG VI SAVKELVENSLSA AS I L	
humPMS2	(57)	KLAEYVLEHESSNECQVEEENFECLTLKHHSIQEFAETVETFEFGEELSSLCALSDVVISCH	140
AtMLH1	(71)	VVFCCLLQONSDCHIRRDLPICERTISDLTKEDPFLSSMGPRGEALASTYVAHVITIT	
Consensus	(71)	LKD GL LI VSD G GI E L KH TSKI F DL L S GFRGEALASL LA VTIST	
humPMS2	(127)	ASAKVETILMFHDHGKIIQKTPYPRPRCTVSTQCESTLPVHEEFRIKKETAPMGOVHAYCISA	210
AtMLH1	(141)	KQQIHCVSYRDGVMHEPKACAAYKQIMGENSYNMIAETITLSSADDCGTTDLSRMAHYN	
Consensus	(141)	G RL F KGT I V NLF L R K Q N DYAKIV LL I	
humPMS2	(197)	GIRVSCINQLGCKRQPVCTGGSPFIKENGGVFEQKQLQSIPFVOLPPSDSVCEEYGLSCSALHNL	280
AtMLH1	(210)	NVSPSCRKH---SAVKADHSVVSRLDSRSTVSVSAKNM---KV---E-----VSSCSSGCT	
Consensus	(211)	I SC G V S SPS D I SVFG LI L LS DA	
humPMS2	(267)	EYISSEFQCTHGVGRSSDTRQFFINRPPCDPAKVCILVNEVHMYNRHQYFVLNLSVDSCEVDIN	350
AtMLH1	(264)	EDMEGHSNSNYVAKKTIL---VLEINDLVECSALKGAIEIHAATLPKASKPEYMSINLPREHVDIN	
Consensus	(281)	F I GFISN H KS FIN R D A L R I VY K PFV L I L E V D I N	
humPMS2	(336)	VIEDRQIILQEEKLLAVLKTSLIGMFDSDVNKLNVQQPLLVEGNLIMHAEDLEKPMVEKQDQSPS	420
AtMLH1	(331)	IHTKEVSLNQEIIIEMIQSEVE-----VLRNENDTRTPCEQKVEYIQ	
Consensus	(351)	I P K K I L III MI S IKL A K E	
humPMS2	(406)	LRTGEEKVSIIRLREAFSLRHTENKHSHPKTPEPRRSLLQKRGMSSTSGAISDKGVLRPQKEAF	490
AtMLH1	(377)	STLTSCSSSPVQKPSG---QKQKVVNKMVRTDSSDEASRLHAFQPKPQLSPDKVSSSVVRSS	
Consensus	(421)	K D IS A T P P G A L L K A V	
humPMS2	(476)	SSSHGSDPTIRAELEKDSGHGSTSVDSEGFSPDTGSHCSSEYAASSPGDRSCSHDSQEKAPETSS	560
AtMLH1	(443)	RQRNEKETALLSSQOE-----LIA--G-----VDSCHPMLTARNCIYVGMADIV	
Consensus	(491)	P D D A V I S G E V DD	
humPMS2	(546)	ESDVCHSNQELGCKFRVLPQPTNLATPNTIRFKKEEISSSDICQKLVTQDMSAQVDVAVKINKKV	630
AtMLH1	(489)	PALEQYN-----SHLYLAN-----VVNLSEELMYQQTERRFAHFNAIQLSDPAPISLILLALKEEDL	
Consensus	(561)	FA V T SK L N I S S L L L	
humPMS2	(616)	VLDFSMSSAKGKQLHHEAQSEGEONYRKRAKCPGENAAEDELKKEISKTFPAEMEIIGQFNELG	700
AtMLH1	(547)	DGNDTKDDKEKRAEMNTLLKEKASMLEEYSVHEDSSAALSRLPVILDQYTPDVRVPSFL--LQCG	
Consensus	(631)	P S L R I L E AE F I N A I S M E I LG	
humPMS2	(686)	FIITKLNDIFIVDQHEIDEKYNFEMLQOHTVLOQRLIAPQTLNLTAVNEAVIENLEIFRKNGEFVI	770
AtMLH1	(615)	NDVEWEDKSCFQGVSAIGNFYAMHPPLLPNPSDGIQFYSKRGESSQEKSDLEGVDMEDNLDCLLS	
Consensus	(701)	I E A F G I SA A L NLDI D L	
humPMS2	(756)	ENAPVTEAKLISLPTSKNITFGPDVDDELIFMSDSPGVMCPRSPQMFASRACKRSVMIGTALNTS	840
AtMLH1	(685)	EAENAWACE-----ESSIQHVLFPQSMRLPKPPASMASNGTFEIVASLEKLYKIFERC-----	
Consensus	(771)	D R WS L L M S V K K K	
humPMS2	(826)	EMKKLITHMGEMDHPWNCPHGRPTMRHIANLGVISQN	877
AtMLH1	(738)	-----	
Consensus	(841)	-----	

FIG. 3

humPMS2	(1)	MERAESSSTEPAAKIDRKSVQICSGOVVLSLSTAKELWENSLDAGATNIDLKLKDYGVLDLIEKSE	70
AtPMS1	(1)	-----MRTKGLPEGVRSMSRSIIIMFDMARVBEELFNSLDAGAKVSIIFGVVSCS-VKIVV	
Consensus	(1)	K IKPI H I SG IM LA V ELV NSLDAGAT I I L I V D	
humPMS2	(71)	NECCVEENFEGTLKHHSIQEADLQVETFGFRGEALSELCAISDVTISCHASAKVETELMFDH	140
AtPMS1	(59)	DESSSRDDLVLGERYASRPHDGTNVEIASETFGFRGEALASISDIISLLEVKAIGRPNSYKVMKG	
Consensus	(71)	G GV D L KH TSK DF L T ETFGFRGEALASI IS L I T G R M	
humPMS2	(140)	NGKIIQKTPYP-PP-RCVNSQQESTLEVEHHEFERNIKREYAKMVQVLHAYCIISAGI-----	210
AtPMS1	(129)	SKCLHLGIDDDKDSCTTITRDLEYSQVVRHYMSSPKVLESIKKCVPRIALVHNSVFSVLDIESD	
Consensus	(141)	I R GTIVSV LF S PVR K Q KK I L II A I	
humPMS2	(199)	-----RVSCTNQLGQGRQPVVCGGSPSIKEIISV	280
AtPMS1	(199)	EELFQTNPSSSAFSLMRDAGTEAVNSLCKVNVTDGMLNVS GFECADDWPTDGOQGRNRRLQSPPYI	
Consensus	(211)	VS K TG I N G I	
humPMS2	(231)	-----GQKQLQSLIPVQLPSSDSVCEYGCSCSDALHNFYIISCFISQCTHVGCRSSTRQF	350
AtPMS1	(269)	LCIACPRRLYE-SFEPKTHVEKKWGVLAFIRITANWKKDRIELFDSGADILAKQRQDLIDKI	
Consensus	(281)	F S I F P A E LA L G G D	
humPMS2	(290)	FFINR-----RPCDPAFVCLVNEVYHMYNRHOYFVVLNISVSECVDINPTDKRQILE	420
AtPMS1	(339)	RLQSGSLFSILHFLDADWPPEAPAKKLKRSNDHAPCSLLFSADFKQDGYFSPRKDWSPECEVE	
Consensus	(351)	N DPAK H FP D V I L	
humPMS2	(346)	QEEKLLAVLKTSLIGMFDVNKLNVSQPLLVVEGNLIKMAADLEKPMVEEDQSPSLFGEEKKDV	490
AtPMS1	(409)	KIQNPKEQGTIVAGFESRTCSLLQSRDIEMTINEFPQVTDLLETSLVADSKCRFLTRCQITFPVNINH	
Consensus	(421)	DS LN I Q D L A L K Q S T	
humPMS2	(416)	SISRLREAFS-----RRTTENKPHSEKTEPRRPLQG	560
AtPMS1	(479)	DFMKDSVDLNFQFQGLKDELVDVSNCTGKHLRGCSRVSLTFHEPKSEVEGYESVVEIMINEKQSPRV	
Consensus	(491)	K D L H P P K S	
humPMS2	(450)	KRGMLSSSTSGAISDGVLRPQKEAVSSSHG--SDPTDPAEKEKDSGHGSVSEGESIPITGSHCSS	630
AtPMS1	(549)	LETREGGSCYCDVYSDPTDPCSLGSSWQDTDFWFTSCCSSDGGGIGEDFNIPIITAEISYSEKVGSKK	
Consensus	(561)	S SDK A S P SDRA V T IDS F D	
humPMS2	(518)	EYAASSPDGRGSQEHVDSQ-----KAEETDDSFSDVDCHSNQEDTGCKFRVLEQTNLATPNTKRFKKE	700
AtPMS1	(619)	YLSSVNVSSSVTGSFCLSSWSPMYSTSATKWESEYQKGRILEQSLRLGRMDSEFCFSAANNIKFHDH	
Consensus	(631)	AA G S S E P SD D K LP P S	
humPMS2	(583)	ILSSSIQKLVNTQMSASQVDVVKVNEK----VVLDFMSMLAKRIKQLHHEACQSEGEENYRK	770
AtPMS1	(689)	EVIPENCQETGDSFTAIONCTQLDEKCSWGHADDVRIDQYSIRIEKFSYMDGTENNAKRSKRS	
Consensus	(701)	EII D C S LA KI K L SI K QN G Q KK	
humPMS2	(649)	AKICPGENQ-----	840
AtPMS1	(759)	SAPPFYREKKRFISLCKSDTKPKNSDPSEPDLECLTQPCNASQMHKCSILDVSYDHIQETEKRLS	
Consensus	(771)	RA	
humPMS2	(659)	-----	910
AtPMS1	(829)	SASDLKASAGCRTVHSETQDEDVHEDFSSEEFLDPIKSTTKWRHNCVAVSQVPKESHELHGQDGVFDISSG	
Consensus	(841)		
humPMS2	(659)	-----AASDELKKEISKIMFAEMEIGFNLGFITKLNEDIFVDCHEIDEKYNFEMCOQHTVLQGQRL	980
AtPMS1	(899)	LLHLRSDSLVPESNRHSLEDAKVLQVDDKKYPIVACGTVAVDCHADERIRLEERTKFINDALI	
Consensus	(911)	A E L I K D II Q FI I IVDQHA DEK E L I A I	
humPMS2	(724)	IAPQTLNLTAVNEAVIENLIFPKNSGDFVDENAPVTERAK-----ISLSTSKNNTFGPQ	1050
AtPMS1	(969)	FVLTLKVPEMGYQLQSYSEQIEDWECNITVEGSTSFKKINMSIIQRKPTPITNAVECILGVNLSDV	
Consensus	(981)	L M LL E R GF I A S K L ALP	
humPMS2	(782)	VDELIFMSSSPVMCRSGRKQMFASRACKSVICTANTSEMKKLTHMGEMDHPWNPCEGRFMR	1120
AtPMS1	(1039)	LLIFLQCAATDSSSTIPSLRLVLNKAAGATFDSLLPSECSLIIDGLQTSLSLFCQAGCRFTV	
Consensus	(1051)	DL E I LADS G P V M SKACR AIM G AL SE II L FNC HGRPT	
humPMS2	(852)	HIANGVISQN-----	1164
AtPMS1	(1109)	PLVDKALHKQIAKLSGRQVWHGLQRREITLDRAKSRLDNAKS-	
Consensus	(1121)	I L I N	

FIG. 4

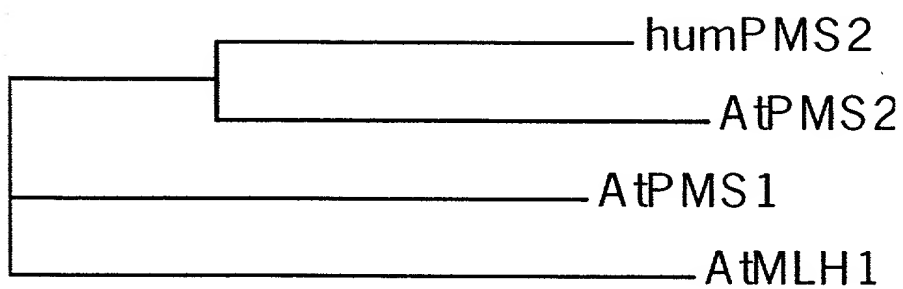


FIG. 5

humPMS134 (1) ATG A GCGAGCT GAGAGCT CGAG ACAGAACT GGT AGGC C-----AT C A C CTA T G T C T G A A G T
 AtPMS134 (1) ATGC AAGGAGT TCTTCTC GCG GACGACG A CTA GCT T C C T T T G A A G C C T A A C A G A A C G
 Consensus (1) ATG A GAG T CG T C CT CTA C AT A ACCTAT A G AA
 71 140
 humPMS134 (65) C G C C A T C A G A T T G C T C T G G G G G G A C T G A G T C T A A G C A T G C G A A G G A G T T A T A E E A A
 AtPMS134 (71) T A T T C A C A G A C T G T C C G T C A A C C A C T T A G A C C T C T T T G G C C G C A G G A G C T T C C G A A
 Consensus (71) A T C A AT T G T C G G C A G T T T CT C G C G T A A G G A G T G T G A A A
 141 210
 humPMS134 (135) C A G T T G G T G C T G C C C A C T A T A T T C T C A A G C T A A G C A G T T C C A T G C T C T A T T G A A T
 AtPMS134 (141) T A G T C G A C G C C C C C C A G C G T A A G A G A T T C C C G A G A C T C C C C A A G C T A T T T C G G T C
 Consensus (141) A G T C T A G C G G C C C A C A T A T G A T A A C T G A C T A G G G A T T T A G T
 211 280
 humPMS134 (205) T C A G C A A T G C A T G T G C G G -----G A A G A G -----A A A C T C G A A G G C T T A A
 AtPMS134 (211) A T T C A C A A T G C T G T G C A T T T C C C A A C C A T T T C A G T T T G T G T C A A T T C C C A A G A A C T T G
 Consensus (211) G A C A A T G G T G T G G T A A A G A A C T C G A A G C T T
 281 350
 humPMS134 (251) -----G T C T C A A C A T C C A C A T C T A A G A T C A A G C T G C C C C A A C C G G T T G A A A C T
 AtPMS134 (281) A T G T T C T T G C A T T C C A T C A T C T C T A A A T A G C G G T T C A G A A T C T T C A A T T G A C T A C T
 Consensus (281) C C T A A C A T C A A C T C T A A G A T T C G A C T T A T T G A A C T T
 351 420
 humPMS134 (311) T T G C T T T C G G G G A A G C T T G A G C T A C T T T G T G C C A A C A C A T T C T A C T C T C C C
 AtPMS134 (350) A T G G T T T A A G A G C A G A A C C T T G A G C T C T T G T G C T T C A A A C C C A T G C G G A A A A A A A A A
 Consensus (351) T G G T T T G G G A A G C T G A G C T C T T G T G C A T G G A T T C A C T A C G C A
 421 444
 humPMS134 (379) G A T C C G C C A G C T T G A A C T ---
 AtPMS134 (420) C A T G A C C A C T T G C T A G C T C
 Consensus (421) G A T G C A G T T G A C

FIG. 6

humPMS134 (1) --MERAEESSTEPAKAKKEDKSVQICSGQVILSSAVKELVENSIDAGATNIDLKIKDYGVLIET 70
 AtPMS134 (1) MQGDSSPTITSSPLRENNVIERICSGQVILSSAVKELVENSIDAGATSEINIRDYGEYFQ
 Consensus (1) D A S S T A I K P I R I H I C S G Q V I L L S S A V K E L V E N S I D A G A T I D I L K D Y G D V

 71 140
 humPMS134 (69) SDNGCGVEEEN-----EGILKHHTSKIQESADLTQVEFGFRGEALSSLCALSDVETISCHA
 AtPMS134 (71) SDNGCGISPTNKKVCVQILRRTFDVILKHHTSKLEDITDLNLITVGFGEALSSLCALGNLVEIRTK
 Consensus (71) DNGCGI NF D L L K H H T S K I D F D L N L T F G F R G E A L S S L C A L L T I T

 141
 humPMS134 (128) SAKYGE
 AtPMS134 (141) NEPTA
 Consensus (141) VAT

FIG. 7

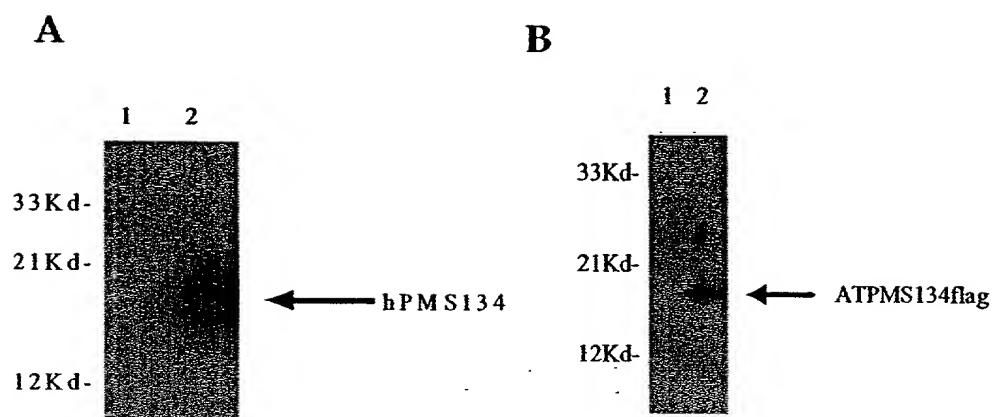


FIG. 8

Dominant Negative Effects of *Arabidopsis thaliana* PMS2 homolog

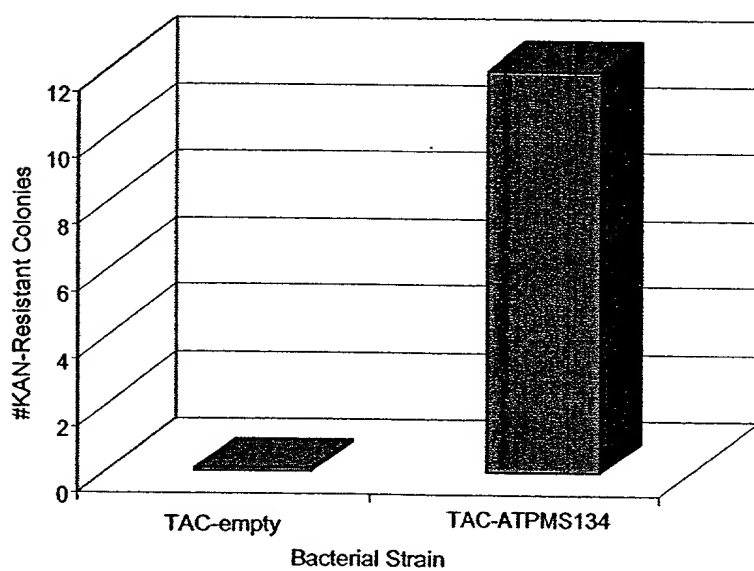


FIG. 9



FIG. 10

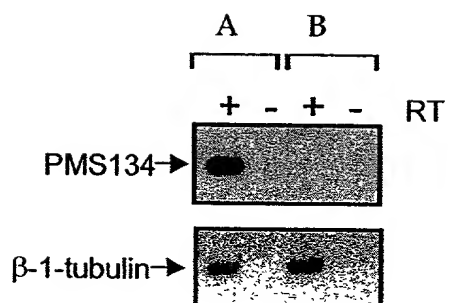


FIG. 11

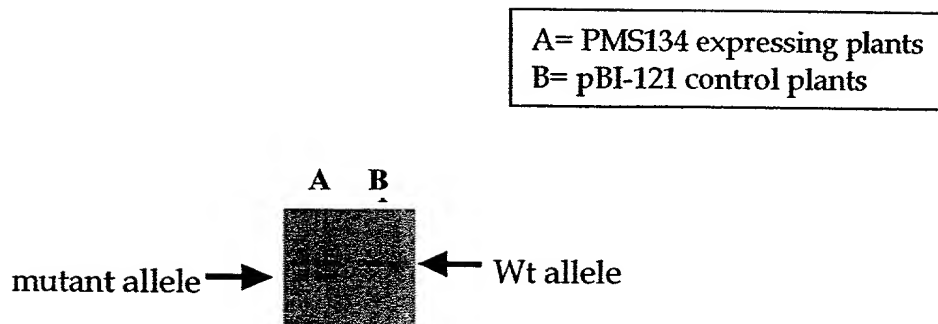
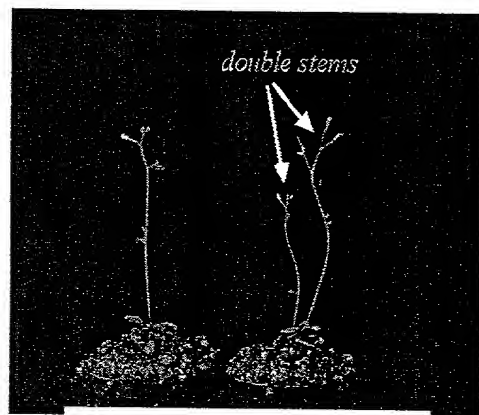


FIG. 12



Normal MMR-

FIG. 13